

E HU SONG/AU 25
L1 56 S (E3)
E ZHONG MIN/AU 25
L2 116 S (E3)
L3 1 S L2 AND SERINE
L4 1 S L3 AND ANTIBOD?
E LADUNGA ISTVAN/AU 25
L5 21 S (E3)

FILE 'MEDLINE, EMBASE, BIOSIS, CAPLUS' ENTERED AT 15:27:28 ON 01 NOV 2006
L6 16410 S SERINE (S) PROTEASE (S) INHIBITOR?
L7 248 S L6 (S) ANTIBOD?
L8 102 DUP REM L7 (146 DUPLICATES REMOVED)
L9 102 SORT L8 PY A



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- Select PubMed under the Links menu to retrieve all records for the MeSH Term.
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1: Serpins

Links

A family of serine proteinase inhibitors which are similar in amino acid sequence and mechanism of inhibition, but differ in their specificity toward proteolytic enzymes. This family includes alpha 1-antitrypsin, angiotensinogen, ovalbumin, antiplasmin, alpha 1-antichymotrypsin, thyroxine-binding protein, complement 1 inactivators, antithrombin III, heparin cofactor II, plasminogen inactivators, gene Y protein, placental plasminogen activator inhibitor, and barley Z protein. Some members of the serpin family may be substrates rather than inhibitors of SERINE ENDOPEPTIDASES, and some serpins occur in plants where their function is not known.

Year introduced: 1990

Subheadings: This list includes those paired at least once with this heading in MEDLINE and may not reflect current rules for allowable combinations.

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 cerebrospinal fluid chemical synthesis chemistry classification
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Do Not Explode this term (i.e., do not include MeSH terms found below this term in the MeSH tree).

Entry Terms:

- Serpin Superfamily
- Superfamily, Serpin

Previous Indexing:

- Enzyme Inhibitors (1968-1978)

- Protease Inhibitors (1979-1989)

Pharmacologic Action:

- Serine Proteinase Inhibitors

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Chemicals and Drugs Category

Amino Acids, Peptides, and Proteins

Proteins

Serpins

alpha 1-Antichymotrypsin

alpha 1-Antitrypsin

Angiotensinogen

Antiplasmin

Antithrombins

Antithrombin III

Heparin Cofactor II

Hirudins

Complement C1 Inactivator Proteins

HSP47 Heat-Shock Proteins

Ovalbumin

Plasminogen Inactivators

Plasminogen Activator Inhibitor 1

Plasminogen Activator Inhibitor 2

Protein C Inhibitor

Thyroxine-Binding Proteins

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OM protein - protein search, using sw model

Run on: October 21, 2006, 01:15:26 ; Search time 615 Seconds
(without alignments)
610.782 Million cell updates/sec

Title: US-09-903-582-2
Perfect score: 1315
Sequence: 1 MKPGGFWLHLLGASLPAA.....YNSDSSLTLREFYMAFRQKC 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query					Description
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1	1315	100.0	246	1	PCT-US02-21670-2	Sequence 2, Appli
2	1315	100.0	246	1	PCT-US04-37982-3430	Sequence 3430, Ap
3	1315	100.0	246	29	US-09-903-582-2	Sequence 2, Appli
4	1315	100.0	246	41	US-11-124-368A-170	Sequence 170, App
5	1292	98.3	243	1	PCT-US02-21670-4	Sequence 4, Appli
6	1292	98.3	243	29	US-09-903-582-4	Sequence 4, Appli
7	1292	98.3	491	41	US-11-166-372-2150	Sequence 2150, Ap
8	1292	98.3	491	41	US-11-166-372A-2150	Sequence 2150, Ap
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11	1292	98.3	842	25	US-09-544-511-16	Sequence 16, Appli
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27	1292	98.3	846	31	US-10-189-940-148	Sequence 148, App
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34	1288	97.9	837	34	US-10-428-275-244	Sequence 244, App
35	1288	97.9	837	39	US-10-971-479-126	Sequence 126, App
36	1287	97.9	842	34	US-10-428-275-276	Sequence 276, App
37	1284	97.6	842	34	US-10-428-275-274	Sequence 274, App
38	1269	96.5	838	1	PCT-US01-04098A-3151	Sequence 3151, Ap Sequence 3151, Ap
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RESULT 3
AAB19727
ID AAB19727 standard; protein; 842 AA.
XX
AC AAB19727;
XX
DT 19-FEB-2001 (first entry)
XX
DE Human SECX Clone 4324229-2 encoded protein.
XX
KW SECX; human; diagnosis; therapy; surface adhesion protein; antitumour;
KW neurological disorder; developmental disorder.
XX
OS Homo sapiens.
XX
PN WO200061754-A2. -102(a)
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US009392.
XX
PR 09-APR-1999; 99US-0128514P.
PR 03-MAR-2000; 2000US-0186592P.
PR 06-APR-2000; 2000US-00544511. -102(e)
XX
PA (CURA-) CURAGEN CORP.
XX
PI Fernandez E, Vernet C, Shimkets R;
XX
DR WPI; 2000-679487/66.
DR N-PSDB; AAA88796.
XX
PT SECX polypeptides and the nucleic acids that encode them, useful for
PT diagnosing, preventing and treating e.g. cancers, inflammation, arthritis
PT and immunological disorders.
XX
PS Claim 1; Fig 8; 143pp; English.
XX
CC The present sequence is that of surface adhesion protein-like variant
CC encoded by SECX Clone 4324229-2 (see AAA88796). High expression was
CC detected in the lung. The invention provides novel SECX polynucleotides
CC (see AAA88789-804) and the secreted or membrane-associated proteins
CC encoded by them (see AAB19720-34). SECX polynucleotides, polypeptides and
CC antibodies can be used in the detection, diagnosis and treatment
CC (including gene therapy) of a broad range of pathological states.
CC Therapeutic indications for targeting 4324299 include selected lung,
CC breast and ovarian carcinomas. 4324299 has similarity to human limbic
CC system associated membrane protein (LAMP) and may therefore be important
CC in nerve growth and differentiation, epilepsy, Alzheimer's disease and
CC schizophrenia. It also shows similarity to portions of human Down
CC syndrome-cell adhesion molecule (DS-CAM2), and may therefore be useful in
CC the detection, diagnosis and therapy of developmental and neurological
CC abnormalities such as Down syndrome, mental retardation,
CC holoprosencephaly, agenesis of the corpus callosum and schizencephaly
XX
SQ Sequence 842 AA;

Query Match 98.3%; Score 1292; DB 3; Length 842;
Best Local Similarity 99.6%; Pred. No. 1.3e-112;
Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKPGGFWLHLLGASLPAALGWMDPGTSRGPDVGVGESQAEEPRSFEVTRREGLSSHNE 60

Qy 61 LLASCGKKFCSRGSRCVLSRKTGEPECQCLEARPSYVPVCGSDGRFYENHCKLHRAACL 120
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Qy 121 LGKRITVIHSKDCFLKGDTCTMAGYARLKNVLLALQTRLQPLQEGDSRQDPASQKRLLVE 180
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Qy 181 SLFRDLDADGNNGHLSSSELAQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYM 240
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Db 181 SLFRDLDADGNNGHLSSSELAQHVLKKQDLDEDLLGCSPGDLLRFDDYNSDSSLTLREFYM 240

Qy 241 AFR 243
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Db 241 AFQ 243